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Using Oats to Map Corn Genes — with Ideas from a Human Project

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Scientists are expecting to isolate and describe the function of 50,000 corn genes between 1998 and 2003—a seemingly daunting task, considering that it took 50 years to map the first 1,000 corn genes.

Vastly more efficient methods for mapping corn genes are needed, and researchers at the University of Minnesota believe they have the answer.

They found that pollinating oats with corn pollen—followed by rescuing the developing embryo onto an artificial culture medium—resulted in oat plants with

half the usual chromosome number. There were no corn chromosomes. They had been eliminated early in embryo development.

They were interested in these plants because they knew that doubling the chromosome number would lead to pure breeding lines useful in oat breeding programs. However, they also found that corn chromosomes were occasionally retained in the embryo-rescued plants. Progenies of these plants are called oat-corn addition lines. They also found that seed would often be found on plants with only one or two corn chromosomes added to a complete oat chromosome set.

LINK TO HUMAN GENETICS

The researchers realized that these plants could be used to generate lines for the efficient mapping of corn genes. Taking a hint from a human genetic project, they proposed to USDA's National Research Initiative (NRI) Competitive Grants Program that irradiating these oat-corn addition lines could produce lines (called radiation hybrids) retaining only a portion of the corn chromosome.

While the presence of a single corn chromosome (in an oat background)

LEFT TO RIGHT: NORMAL OAT,
CORN, OAT-CORN CHROMOSOME 3
ADDITION LINE.



USDA

The power of radiation hybrid lines for mapping is phenomenal.

reduces the complexity of the corn genome 10-fold, the radiation hybrids would be even less complex. While isolated corn genes could be placed to chromosomes by molecularly hybridizing them with the DNA of the various addition lines, they could be placed to a portion of the chromosome by hybridizing them to the DNA of the various radiation hybrid lines containing portions of that chromosome.

The NRI grant was to be used in part to derive the various oat-corn addition lines and to produce a preliminary set of radiation hybrids to test the potential efficiency of this mapping system. The researchers were able to derive and obtain seed from several plants with the completely normal set of oat chromosomes plus a single pair of 7 of the 10 possible corn chromosomes. Progeny tests indicate these lines have stable inheritance of the corn chromosome pair.

NSF GRANT

At about this time, the National Science Foundation (NSF) announced the new Plant Genome Research Program. The researchers requested funds to develop a complete set of 10 oat-corn chromosome addition lines and 100 radiation hybrid lines per chromosome.

The power of radiation hybrid lines for mapping is phenomenal. Theory indicates that a well-defined set of such radiation hybrids could allow the placement of corn genes to a small DNA segment. Considering that the corn genome is composed of

2.5 billion base pairs, the ability to place a gene to such a short segment through an efficient, straightforward method should simplify placement of the 50,000 genes of corn expected to be isolated by 2003.

The \$1.8 million NSF grant is focused on developing a radiation hybrid mapping system for the genetic and physical mapping of corn genes. However, these lines have many more uses, including the search for corn genes that will improve the productivity or quality of oats, the study of gene expression and interaction when in a new genetic environment, the study of chromosome behavior, and many other applications.

IMPACT

The genome of corn is as large and complex as the human genome. Radiation hybrid mapping of the human genome has placed more than 15,000 genes on the human map. Although the human radiation hybrid lines were derived by fusing individual human cells with rodent cells (mouse, chinese hamster) and cloning in cell cultures, the corn mapping program proposed by the researchers is the same in concept as—and benefits from the successes of—the human genome project.

This project is also a good example of how a broad genome program across various federal funding agencies can complement and advance the application of genomics to agriculture.

The research reported in this factsheet was sponsored by the Plant Genome Program of the Plants Division of the National Research Initiative Competitive Grants Program. To be placed on the mailing list for this publication or to receive additional information, please contact the NRI (202/401-5022 or NRICGP@reeusda.gov). The factsheet also is accessible via the NRI section of the Cooperative State Research, Education, and Extension Service website (<http://www.reeusda.gov/nri>).

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